SHORT COMMUNICATION

Zinc transporter (ZnT)8_{186–194} is an immunodominant CD8⁺ T cell epitope in HLA-A2⁺ type 1 diabetic patients

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Abstract

Aims/hypothesis Anti-zinc transporter (ZnT)8 autoantibodies are commonly detected in type 1 diabetic patients. We hypothesised that ZnT8 is also recognised by CD8⁺ T cells and aimed to identify HLA-A2 (A*02:01)-restricted epitope targets.

Methods Candidate epitopes were selected by ZnT8 plasmid DNA immunisation of HLA-A2/DQ8 transgenic mice and tested for T cell recognition in peripheral blood mononuclear

cells of type 1 diabetic, type 2 diabetic and healthy participants by IFN- γ enzyme-linked immunospot.

Results White HLA-A2⁺ adults (83%) and children (60%) with type 1 diabetes displayed ZnT8-reactive CD8⁺ T cells that recognised a single ZnT8_{186–194} (VAANIVLTV) epitope. This ZnT8_{186–194}-reactive fraction accounted for 50% to 53% of total ZnT8-specific CD8⁺ T cells. Another sequence, ZnT8_{153–161} (VVTGVLVYL), was recognised in

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20% and 25% of type 1 diabetic adults and children, respectively. Both epitopes were type 1 diabetes-specific, being marginally recognised by type 2 diabetic and healthy participants (7-12% for ZnT8₁₈₆₋₁₉₄, 0% for ZnT8₁₅₃₋₁₆₁). *Conclusions/interpretation* ZnT8-reactive CD8⁺ T cells are predominantly directed against the ZnT8₁₈₆₋₁₉₄ epitope and are detected in a majority of type 1 diabetic patients. The exceptional immunodominance of ZnT8₁₈₆₋₁₉₄ may point to common environmental triggers precipitating beta cell autoimmunity.

Keywords Autoimmunity · Beta cell · Environment · Islet · SCL30A8 · Type 1 diabetes

Abbreviations

ELISpot Enzyme-linked immunospot

IA-2ic Intracellular part of protein tyrosine

phosphatase 2

MAP Mycobacterium avium paratuberculosis

PBMC Peripheral blood mononuclear cell

PD Pyruvate dehydrogenase SFC Spot-forming cells ZnT Zinc transporter

Introduction

The autoimmune cascade leading to beta cell destruction in type 1 diabetes is propagated by T cell recognition of specific epitopes. Epitope mapping is therefore critical for staging of autoimmunity during the disease, and for developing and monitoring immunomodulatory therapies. Indeed, a combination of multiple epitope markers is likely to track beta cell autoimmunity more efficiently than any single epitope. Likewise, restoring immune tolerance to a broad antigen spectrum may be clinically more effective [1].

Zinc transporter (ZnT)8 was recently identified as a major type 1 diabetes antigen, with 60–80% of recent-onset type 1 diabetic participants harbouring antibodies against its C-terminal domain [2]. As for other beta cell antigens, such auto-antibodies are likely to be accompanied by autoreactive T cells targeting ZnT8 [1]. Indeed, ZnT8-reactive CD4⁺ and CD8⁺ T cells were recently described in white and Chinese type 1 diabetic patients, respectively [3, 4]. Given their central role in beta cell autoimmunity [5, 6], further characterisation of these CD8⁺ T cells is needed. Here, we identify a highly immunodominant ZnT8_{186–194} epitope recognised by such cells.

Methods

ZnT8 peptide library We synthesised 70 nonamer peptides (>75% purity; ProImmune, Oxford, UK) that had been

selected as potential binders to HLA-A1, -A2, -A3, -A24, -B7 and -B8 (electronic supplementary material [ESM] Table 1). Binding to recombinant HLA-A2 molecules was assessed using Class I REVEAL assays (ProImmune). Candidate epitopes were re-synthesised at >90% purity.

DNA immunisation HLA-A2/DO8 transgenic (A*02:01/ $DQB1*03:02) H-2D^{b-/-}\beta_2 m^{-/-}IA^b\beta^{-/-}IA^b\alpha^{-/-}IE^b\beta^{-/-}$ mice were obtained by crossing HLA-A2 and HLA-DQ8 transgenic mice [7, 8]. These mice were pretreated with cardiotoxin and vaccinated twice with non-coding plasmid or plasmid encoding full-length human ZnT8 (1:1 mixture of Arg/Trp₃₂₅ isoforms) cloned into pcDNA3.1, as described previously [7]. The study was approved by the local ethics committee. Splenocytes were plated $(5 \times 10^5/\text{well})$ in IFN-γ enzyme-linked immunospot (ELISpot) plates (Millipore, Molsheim, France) along with peptides (10 µmol/l). After culturing for 20 to 24 h, plates were treated with a biotinylated anti-IFN-y antibody (U-CyTech, Utrecht, the Netherlands), alkaline phosphatase-conjugated streptavidin and NBT-BCIP (Sigma, Lyon, France). Triplicate wells were counted and averaged using a Bioreader 5000 Pro-SF equipment (BioSys, Karben, Germany).

Study participants We recruited the following participant groups in Paris and Turin: (1) new-onset autoantibodypositive type 1 diabetic adults (n=12; 8 men, 4 women; median age 31 years [range 24-60]; diabetes duration 39 days [0-140]) and children (n=10; 6 boys, 4 girls; median age 12 years [1-16]; diabetes duration 5 days [0-80]); (2) type 2 diabetic patients (n=24; 15 men, 9 women; median age 60 years [12–77]; diabetes duration 12 years [0– 42]); and (3) healthy controls (n=27; 12 men, 15 women; median age 36 years [22-60]). Serum antibodies were measured by RIA, using ³⁵S-labelled GAD65, the intracellular part of protein tyrosine phosphatase-2 (IA-2ic) and ZnT8 (construct C-term CRCW JH6.2). All participants were HLA-A2⁺ (HLA-A*02:01) by genotyping and gave written informed consent. Local ethics committees approved the study.

ELISpot assays Peripheral blood mononuclear cells (PBMCs) prepared as described previously [5] were used fresh or frozen-and-thawed with similar results [5, 9]. PBMCs $(3\times10^5/\text{well})$ were seeded in anti-IFN-γ-coated ELISpot plates in AIM-V medium (Life Technologies, Saint Aubin, France) containing 0.5 ng/ml IL-7 and 10 μmol/l peptide. A viral peptide mix (Flu MP₅₈₋₆₆, Epstein–Barr virus BMLF₂₈₀₋₂₈₈, cytomegalovirus pp65₄₉₅₋₅₀₃) and phytohaemagglutinin (1 μg/ml) were used as positive controls. Pyruvate dehydrogenase (PD)₅₋₁₃ and DMSO diluent were negative controls. After 20 to 24 h, plates were developed and counted as above. For blocking experiments, anti-CD8



(OKT8, 25 µg/ml) or anti-HLA-A2 (BB7.2, 50 µg/ml, both in-house) were added to wells. Readouts are expressed as spot-forming cells (SFC)/ 10^6 PBMCs after subtracting background responses against PD_{5–13} and no peptide (which were identical in all cases). The positive cut-off was set at 3 SD above the average background, as determined by receiver-operator characteristics analysis [5]. Intra- and inter-assay CVs are 14% and 9%, respectively [5].

Statistics Values are expressed as mean±SD or median (range), according to distribution. Comparisons between proportions were made with Fisher's exact test.

Results

We used DNA immunisation [7] to pinpoint naturally processed and presented HLA-A2-restricted epitopes derived from ZnT8 (Fig. 1a). Based on positive responses (i.e. >3

SD above background) in >15% (≥2/12) of immunised mice, ten candidates were selected (Fig. 1b, ESM Table 1). None was positive in control immunised mice. Similar results were obtained using HLA-A2 transgenic mice lacking the DQ8 transgene [7] (data not shown). Most candidate epitopes were located in the fourth transmembrane region (3/10) or in the C-terminal domain (3/10). None overlapped with the Arg/Trp₃₂₅ polymorphic region.

Binding assays to recombinant HLA-A2 molecules were performed in parallel (Fig. 1c). While most (8/10; 80%) candidate epitopes identified by DNA immunisation were strong HLA-A2 binders, two epitopes (number 50, ZnT8_{253–261} and number 57, ZnT8_{280–288}) were weak binders. In addition, several epitopes (22/30; 73%) that were strong HLA-A2 binders did not elicit significant responses in DNA-immunised mice. Thus, compared with epitope selection based on HLA-binding affinity, DNA immunisation allowed us to focus on fewer candidates (10/70 vs 30/70; 14% vs 43%), including two weakly binding

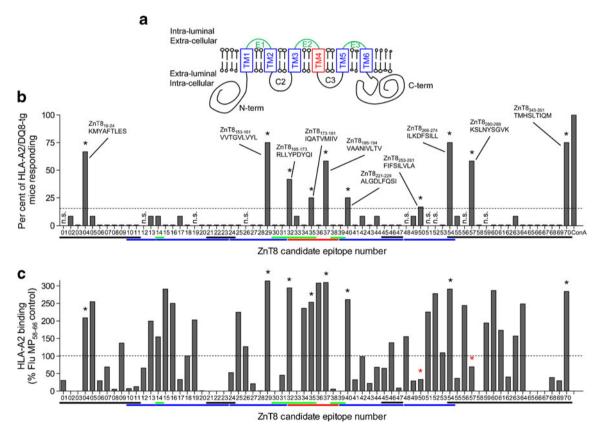


Fig. 1 HLA-A2-restricted ZnT8 candidate epitopes. **a** ZnT8 protein structure and topology. The three intra-luminal loops are shown in green, the four extra-luminal domains in black and the six transmembrane (TM) domains (TM1–TM6) in blue, except TM4 (red). **b** ZnT8 candidate epitopes selected by DNA immunisation in HLA-A2/DQ8 transgenic (tg) mice (n=12). Splenocytes were restimulated in vitro with the 70 peptides listed in ESM Table 1. Bars represent the per cent of mice responding to the designated peptide or to concanavalin A positive control. The dotted line represents the positive cut-off (>15%

of mice responding). Selected epitopes are indicated by asterisks. Coloured lines (*x*-axis) show the position of each epitope within the ZnT8 structure, according to the colour code above (**a**). **c** Binding of ZnT8 peptides to recombinant HLA-A2.1 in vitro. The same peptide library was tested using the Class I REVEAL binding assay (Proimmune). Results are expressed as per cent binding; the dotted line shows the positive cut-off (>100% binding compared with the reference Flu MP₅₈₋₆₆ peptide). Asterisks indicate peptides selected by DNA immunisation, two of which (red) are weak binders



peptides. Moreover, DNA immunisation selects candidates on the additional criterion of natural processing and presentation [7].

The identified peptides were subsequently tested for CD8⁺ T cell recognition using PBMCs from type 1 diabetic, type 2 diabetic and healthy participants. Results are summarised in Fig. 2a and raw data in ESM Figs 1 and 2. All but one peptide (ZnT8_{221–229}) were recognised by PBMCs of at least one type 1 diabetic patient. ZnT8_{153–161} (number 29; VVTGVLVYL) and ZnT8_{186–194} (number 37; VAANIVLTV) emerged as immunodominant. ZnT8_{153–161} was recognised in 25% of type 1 diabetic adults and 20% of type 1 diabetic children, but not by type 2 diabetic and healthy participants.

ZnT8_{186–194} was targeted in 73% of type 1 diabetic patients, without significant differences between adults (83%) and children (60%). PBMCs from type 2 diabetic patients and healthy controls rarely recognised this epitope (12% and 7%, respectively; $p \le 0.009$ for both compared with type 1 diabetic adults or children), while ZnT8_{253–261} (number 50; FIFSILVLA) was more frequently recognised in type 2 (25%) than in type 1 diabetic (8% adults, 10% children) and healthy participants (0%; p=0.007 for comparison between type 2 diabetic and healthy). ZnT8_{153–161} and ZnT8_{186–194} were strong HLA-A2 binders, were located in transmembrane regions and positive in 75% and 58% of immunised mice, respectively. IFN-γ ELISpot assays

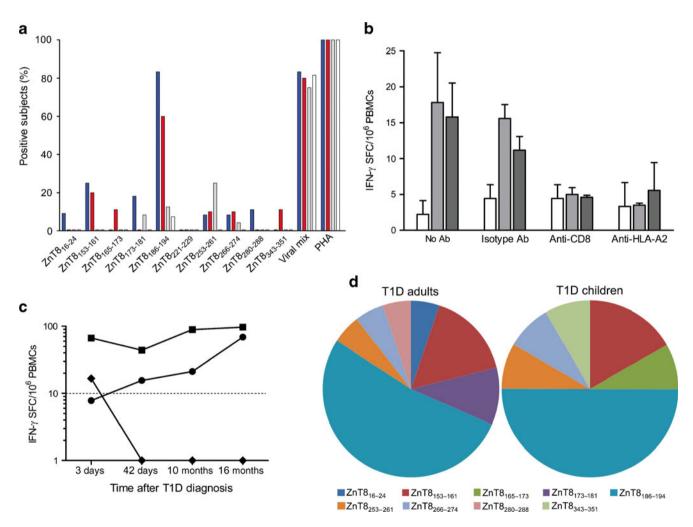


Fig. 2 Recognition of HLA-A2-restricted ZnT8 epitopes in different study participants. **a** Per cent of new-onset type 1 diabetic adults (blue bars; n=12) and children (red bars; n=10), and of type 2 diabetic (grey bars; n=24) and healthy participants (white bars; n=27) responding to each individual epitope by IFN- γ ELISpot. **b** IFN- γ ELISpot responses were measured in a type 1 diabetic adult using PBMCs stimulated in the presence of no antibody (Ab), isotype control antibody, anti-CD8 or anti-HLA-A2 antibody. Counts (mean±SD) of triplicate wells are given without background subtraction for each of the indicated peptide stimuli, i.e. no peptide (white bars), ZnT8₁₈₆₋₁₉₄

(light grey bars) and ZnT8₂₅₃₋₂₆₁ (dark grey bars). **c** Patient A03 was tested at four subsequent time-points for PBMC reactivities against the peptides ZnT8₁₈₆₋₁₉₄ (circles) and ZnT8₁₅₃₋₁₆₁ (diamonds), and the viral mix (squares). Results are expressed as mean IFN- γ SFC/10⁶ PBMCs and are background-subtracted. **d** Relative distribution of epitope specificities in type 1 diabetic (T1D) adults and children as indicated. The per cent prevalence of each epitope out of all epitopes recognised among new-onset type 1 diabetic adults (n=19) and children (n=12) is shown



(*n*=14) were performed using two different ZnT8₁₈₆₋₁₉₄ peptide batches and yielded identical results in 13 (93%) of 14 assays. Moreover, reactivity to ZnT8 epitopes was neutralised by anti-CD8 and anti-HLA-A2 antibodies (Fig. 2b), demonstrating that IFN-γ responses originated from CD8⁺ T cells that recognised HLA-A2-restricted epitopes. As previously observed for GAD- and IA-2-reactive CD8⁺ T cells [5, 7] and for ZnT8-reactive CD4⁺ T cells [3], there was no correlation between anti-ZnT8 T cell and autoantibody responses (data not shown).

The median frequency of ZnT8 epitope-reactive CD8⁺ T cells in new-onset type 1 diabetic patients (34.5 SFC/10⁶ PBMCs, i.e. 0.003%, range 0.0007–0.08%) was similar to that previously observed for other beta cell epitopes [5, 7]. Moreover, one type 1 diabetic adult patient (identified as A03) was studied at four different time points (Fig. 2c). While IFN- γ responses to a viral mix remained fairly stable over time, frequencies of ZnT8_{186–194}-reactive T cells secreting IFN- γ gradually increased over time, while the corresponding ZnT8_{153–161}-reactive T cells rapidly disappeared.

The immunodominance of ZnT8₁₈₆₋₁₉₄ was also evident when considering its relative representation among all epitopes recognised (Fig. 2d). Indeed, ZnT8₁₈₆₋₁₉₄ was the most frequently targeted peptide in type 1 diabetic adults and children (53% and 50% of total ZnT8-reactive CD8⁺ T cell responses, respectively) compared with other epitopes.

Discussion

ZnT8 is clearly a major target of autoreactive CD8⁺ T cells in white new-onset type 1 diabetic patients. Strikingly, a single HLA-A2-restricted ZnT8₁₈₆₋₁₉₄ epitope was recognised by the overwhelming majority of ZnT8-reactive T cells (50–53%), and in both type 1 diabetic adults (83%) and children (60%). Another epitope, ZnT8₁₅₃₋₁₆₁, ranked second, being recognised in 20% to 25% of type 1 diabetic patients. Such a high degree of epitope focusing is surprising, as autoreactivity is usually more widely distributed against different sequences [5]. Indeed, the two most immunodominant epitopes described to date are GAD₁₁₄₋₁₂₃ [5] and preproinsulin (PPI)₁₅₋₂₄ [6], which are recognised in ~50% of type 1 diabetic adults compared with the 83% scored by ZnT8_{186–194}. An increase in ZnT8_{186–194}-reactive IFN-γ responses during the disease was also observed in one patient, contrary to observations for most epitope reactivities, including ZnT8₁₅₃₋₁₆₁, which rapidly wane after diagnosis [9]. ZnT8_{253–261} was recognised in 25% of type 2 diabetic patients, a population seldom included in previous T cell studies. The phenotype of these patients was not distinctive; they were all antibody-negative and all but one not being treated with insulin. However, it is possible that larger ad hoc studies focusing on patients of uncertain classification may reveal a discrete subset.

The epitopes here identified do not overlap with those targeted by CD4⁺ T cells [3]. The subdominant ZnT8_{153–161} epitope was also recognised by PBMCs of Chinese HLA-A2⁺ recent-onset type 1 diabetic patients [4]. In contrast, the novel ZnT8₁₈₆₋₁₉₄ emerges here as the major epitope recognised. Intriguingly, we recently described the same ZnT8_{186–194} epitope and its contiguous ZnT8₁₇₈₋₁₈₆ sequence as targets of autoantibody responses in ~60% of Sardinian type 1 diabetic patients [10]. These autoantibodies were cross-reactive with homologous sequences of the Mycobacterium avium paratuberculosis (MAP) 3865c protein, prompting the hypothesis that MAP could be an environmental trigger of type 1 diabetes via a molecular mimicry mechanism [10]. It would therefore be relevant to investigate whether ZnT8_{186–194}-reactive CD8⁺ T cells also cross-recognise MAP3865c_{133–141}, which, if confirmed, could explain their high prevalence.

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Duality of interest The authors declare that there is no duality of interest associated with this manuscript.

Contribution statement MS and GA designed and performed experiments, participated in data analysis and interpretation, and edited the manuscript. EL and CB participated in study design and data interpretation, provided blood samples and clinical data, and edited the manuscript. CR, JCC, DDL, BB, DL, JFG, OL and GB participated in research discussions, provided blood samples and clinical data, and reviewed the manuscript. FAL and LAS participated in the study design and data interpretation, provided reagents and reviewed the manuscript. JCH and HWD participated in the study design, data analysis and interpretation, performed experiments, provided reagents and edited the manuscript. RM coordinated the study, designed experiments, participated in data analysis and interpretation, and wrote the manuscript. All authors gave final approval for the article.

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